

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCCTTCGCCATCGCCCCGC
GTTTGGCCCAGGACGGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAACTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCCCTGC
ATTACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCCTGCT
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGAAGACCAAGATATTTTTTCTCTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS
SRKQQNVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLTDINVKAPALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

103696-103701

FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGCGGGCG
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC
GCGGCTGGAGGAGGAGAACCAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC
AGAGCGACCCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGGG
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCTGCCTCCCGGGTCCTTTGTGCCTCGACCTCATA
AGCCCCCTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCCGCTGCCTGCCTCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCCGCC
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCAGCCCCAG
GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCCCTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
AGAGCAGTTGGTGGGAGCAAGGCCGAGTTCAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG
GCGGCTGGCCAGGCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
TTGGCGAGCTGGTCCGCACAGGAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGCAGGAGGGTCTGCTG
CGGCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGAGCGGCTGGTGTCACTGTCTG
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGGACA
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA
GAGATCGCGGCTTCCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
CATGCCGCCAGCGGGTGCTTCGGGCCCTCAGCCTCGTTGCTGTCCCAGTGCGAGATGAACCTCATGGCC
AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGGAACTGGAGATGCAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAAGTGGGCCGTT
ACATGTGGATAAACCCAGGAAGTGAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
GGGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC
ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT
TGGTCCACGCTCCGTTACCCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCC
GAGGAAGTGGAGCAGCGGGAGGCGGCTGAGCCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG
CCTGCCCTGGAACTTTGGGCCTTTGTCCAAGCCCCGGCGGGAAGTGCAGCAGAGCCAGCCCGGGGATGA
TTGATGTCCGGAAAAACCCCTGTAAAGCCCTCGGGGCAGACCCTGCCTTGGAGGGAGACTCCGAGCCT
GCTGAAAGGGGCAGCTGCCTGTTTGTCTTCTGTGAAGGGCAGTCTTACCACACCCCTAAATCCAGG
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCCCAAAAGAACTGGACCCTCATTT
AACAAAATAATATGCAAATCCCACCACTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCCTTGTG
TCTTGCTCGAATCTCAGGACAATCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTTCAGGGGTTTG
GCCAAGAATCATCACGAAAGGGTCGGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG
GAAACTGGGAGACTTTAGGATCTTAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

1003996.12201

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLNLNGLPPGSFVPRPHTAPLGGAHAHV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPELCLLELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRLEETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQORRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS
LRQEKDSLKQRLEIDGKLRQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLRREEQHQQQIAFSELEMQLLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRROYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGGEKRSKLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

1002296 "12701
1002296 "12701

FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCACATTTACCATCT

102996-42701

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSLWLCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISR SCTRNRHVLYP

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

100296 12701

FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGTCTGGAGAGCTCCCCG
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGCTCTCG
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCG
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG
TCGCCGGCCCGGCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCCGCTGCTACCCCTG
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCGCCC
GCCCCGCCGGGACGTGGTAGGGG**ATG**CCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC
CCCGCAGGCGGAAGCCCTGGCCGCAGCCGCCAGGACGCGATTGGCCCCGGAACCTCGCGCCCA
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGAATAACGTGGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT
GTGCACCGAGGAGGGGCGCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
TCCACGTGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAACTGCTTTGCAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATG**TAG**ACGCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA
CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA
TTGTTGGTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL
GRPARDEGGSGRDWKSksGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTTPQAEALA
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPL
CAQPECPRLLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWR
IERQAMCTRHECRQM

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGTTTGGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTT
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATCTACTCACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG
GCTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGCG
CTCGTCGCTCAGCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
TGTCGGGGCCCCGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGCTGGTTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGCCCCGCGGTCCAGGGATGGCGGGGCTAGTAGTACCG
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCCTTCTGCAGGGGCTGTGGCAGCACTACCACCCTGGC
TTGCCCGCCCGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTTGTACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCT
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTCACCTG
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATG
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAGAGGATATGGGTAT
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA
GCGTACAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGC
CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAATTCC
GAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCA
TTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGA
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTATGAGTAACTGAAGAACATTTTT
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATT
ACAGGAAGCTTTTATATTAAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTC
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAA
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATCTTTCCTAC
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAAAGTGCT
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACCTGATTGAACTGTCTAGGAACCTTAC
AGATTGTTCTGCAGTTCTCTCTTCTTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA
TGAAAATAAATATTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCTT
TTTACTTCTAGGAAGTCTCAAAAGACCATCTTAAATTAATTATATGTTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTCATTCTGT
CACTTGGCTTCGATTTTTATATTTTCTTATTATATGAAATGTATCTTTTGGTTGTTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA
TAAAGAAAATCTTGTGACTTTAAAAA

	2012	2011	2010	2009	2008	2007	2006	2005	2004	2003	2002	2001	2000	1999	1998	1997	1996	1995	1994	1993	1992	1991	1990	1989	1988	1987	1986	1985	1984	1983	1982	1981	1980	1979	1978	1977	1976	1975	1974	1973	1972	1971	1970	1969	1968	1967	1966	1965	1964	1963	1962	1961	1960	1959	1958	1957	1956	1955	1954	1953	1952	1951	1950	1949	1948	1947	1946	1945	1944	1943	1942	1941	1940	1939	1938	1937	1936	1935	1934	1933	1932	1931	1930	1929	1928	1927	1926	1925	1924	1923	1922	1921	1920	1919	1918	1917	1916	1915	1914	1913	1912	1911	1910	1909	1908	1907	1906	1905	1904	1903	1902	1901	1900	1899	1898	1897	1896	1895	1894	1893	1892	1891	1890	1889	1888	1887	1886	1885	1884	1883	1882	1881	1880	1879	1878	1877	1876	1875	1874	1873	1872	1871	1870	1869	1868	1867	1866	1865	1864	1863	1862	1861	1860	1859	1858	1857	1856	1855	1854	1853	1852	1851	1850	1849	1848	1847	1846	1845	1844	1843	1842	1841	1840	1839	1838	1837	1836	1835	1834	1833	1832	1831	1830	1829	1828	1827	1826	1825	1824	1823	1822	1821	1820	1819	1818	1817	1816	1815	1814	1813	1812	1811	1810	1809	1808	1807	1806	1805	1804	1803	1802	1801	1800	1799	1798	1797	1796	1795	1794	1793	1792	1791	1790	1789	1788	1787	1786	1785	1784	1783	1782	1781	1780	1779	1778	1777	1776	1775	1774	1773	1772	1771	1770	1769	1768	1767	1766	1765	1764	1763	1762	1761	1760	1759	1758	1757	1756	1755	1754	1753	1752	1751	1750	1749	1748	1747	1746	1745	1744	1743	1742	1741	1740	1739	1738	1737	1736	1735	1734	1733	1732	1731	1730	1729	1728	1727	1726	1725	1724	1723	1722	1721	1720	1719	1718	1717	1716	1715	1714	1713	1712	1711	1710	1709	1708	1707	1706	1705	1704	1703	1702	1701	1700	1699	1698	1697	1696	1695	1694	1693	1692	1691	1690	1689	1688	1687	1686	1685	1684	1683	1682	1681	1680	1679	1678	1677	1676	1675	1674	1673	1672	1671	1670	1669	1668	1667	1666	1665	1664	1663	1662	1661	1660	1659	1658	1657	1656	1655	1654	1653	1652	1651	1650	1649	1648	1647	1646	1645	1644	1643	1642	1641	1640	1639	1638	1637	1636	1635	1634	1633	1632	1631	1630	1629	1628	1627	1626	1625	1624	1623	1622	1621	1620	1619	1618	1617	1616	1615	1614	1613	1612	1611	1610	1609	1608	1607	1606	1605
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRLQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
OMLLNEKVLPLAYSOETVSFYEDLKNHYKDILOSCOTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCCTGACTTCTTCCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACGTCTTGCATCATTACGGATTTCG
AGACAAGTGACCCAGGATCGAGTGGGAAGAAAATTCAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCAGTCCCACGGATT
CCAGAGCCAATCCAGATTTTCGAATTTCTTCTTTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTTCAGTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATGGGGGGGTTCTGGTTGTCTTGTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCAATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTAATCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGTCTACGTAAACGCCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCAACCACTGGTCTG
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTAAATAACCTATTTTTTTAAAAAGATTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTTCT
CACACAAGTTTTTAGCCTTTTTTACCAAGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCAGTGTTCCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAAGTCAAGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTTTATACTTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTTGCCGAGGCCGCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTAACACACCGTAATTTGGCATTTGTTTAAAC
CTCATTTATAAAAGCTTCAAAAAACCCA

FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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FIGURE 15

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
ATCTTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG
GAGAAGCCACTGCCCCACCGCTTCTCGTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG
CGCATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGACGAGCTGCTGCTG
TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTTGGACCAGGCAGTGGCCCCAC
GACCCCACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCACCTGGTGGAGGTCCAGCATGAGCGC
GGCGCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCTGCCGCCCGCCGAGACAGCACAGAGGCA
CCCAAACCAAAGAGCAGCCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG
GGCCCTGAGGACGACCTGGCTGGCATGTTCTTCCAGATTTTCCCGCTCAGCCCGGACCCTCGGTGGCAGAGCTCC
AGTCCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCGCTGCTCCAGGGCAGCCCC
GAGGTGCCGGGCATCACGGTGCCTGCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG
GTGATGTCCATGCACCGTAGCCACTTCTTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG
CCACAGGACACCGGCTTCTCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
GTGGAGGGCGGGCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCTCAGCCGGGCGCAGGCTCAGTGAT
GTGCGAGGGGGCTCTGCGCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTCACTCCACCGTC
CGTGCCGTCATCGCCACCCTGAGGTCTGGGGAGCAGTGACGCTGGAGCCGGACCTGATCAGCAAAGTCTCCAG
GGGCTGATCAGGTTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
TCCCCGTTTCCAGCCTGTAAGCCCCGTTGTGGTGGTGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCTCTTAGTGGACTGG
CTGGAAATGCTGGACCCCGAGGTGGTCAAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGGAGGAAG
GGCAAAGTCAAGGCCAGGTGCCCTCGTTCCTGCTGAGCCCTTACCTCCTGACCCCTTTACGCATCAGTCCAGCTGGCCC
ACACTGCACCACTGCATCCGAGTCTGCTGGGCAAGAGCCGGGAACAGAGGTTTCGACCCCTCTGCCTCTCTGGAC
TTCTCTGGGCCCTGCATCCATGTTCTTCTGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAGCGGGGAG
GAGCTGGTGTGCTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG
AGCCAGGACGGGGACACAGCCGCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTCAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA
AGGCGCTGCCGAGACCTTCTCTGAGCTCTACCTACAGCGGCCGAGCTGCGGGTGCCCGTGCCTGAGGTCTTA
CTGCACAGCGAAGGGGCTGCCAGCAGCAGCTGCAAGCTGGACGGACTCATCCACCGCTTCATCAGCTCCTT
GCGGACACCAGCGACTCCCGGGCGTTGGAGAACCAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCTGCACGGCCGACCCACCTCAACTTC
CAGGAGTTCCGGCAGCAGAACCACCTGAGCTGCTTCTGACGCTGTGGGCTGCTGGAGCTGCTGCAGCCGCAC
GTGTTCCGCAGCGAGCACCAGGGGCGCTGTGGGACTGCCCTTCTGTCTTCATCCGCTGCTGCTGAATTACAGG
AAGTCTTCCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGAGTTTCATCCATAAGTACATTACCTACAATGCC
CCAGCAGCCATCTCCTTCTGAGAACGACGCCGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG
ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCTGGACGAAGAG
GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTCAAGCTCTCCCTGTTTACCCCTCTGACCGCGGCCGAG
ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
GAGTGTGTCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTCAGCCGCTTTC
CTGCCCACGTTTCATGTACTGCTGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG
TACGCTCTCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCTGGTGGGCATGTACGGCCAGATG
GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGAGCCTGTGGCAGCCGA
CCCCCTCCAAAGCCCCGGCCCGTCCCGTCCCCGGGGATCTCGAGGCAAAGCCAGGAAGCGTGGGCGTTGCTGG
TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG
CTCCGGGCGCGGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTACCTTCTGGGCCACAGCCCTGCCGCGG
AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM
IRSEVLRLVDAALQDLEPQQLLFVQSFQIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVLQLQMLQWLDSFG
VEGGPLRAQLRMLASQASAGRRSLDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSSLLLQEEEPLA
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIQVLLGKSREQRFDPASLDFLWACIHVPRIWQGRDQRTPOKR
REELVLRVQGPPELISLVELILAEATRSDGDTAACSLIQARLPLLLSCCCGDDSVRKVTE
HLSGCIQQWGSVLGRRCRDLLQLYLQRPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMAALLHGRTHLNFQEFRQQNHL
SCFLHVLGLLELLQPHVFRSEHQALWDCLLSFIRLLNRYKSSRHAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDIDMSRRRPEILSFFSTNLQRL
MSSAECCRNLAFLSLALRSMQNSPSIAAFLPTFMCLGSQDFEVVQTALRNLPYALLCQE
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

10.12	10.12
10.13	10.13
10.14	10.14
10.15	10.15
10.16	10.16
10.17	10.17
10.18	10.18
10.19	10.19
10.20	10.20
10.21	10.21
10.22	10.22
10.23	10.23
10.24	10.24
10.25	10.25
10.26	10.26
10.27	10.27
10.28	10.28
10.29	10.29
10.30	10.30
10.31	10.31
10.32	10.32
10.33	10.33
10.34	10.34
10.35	10.35
10.36	10.36
10.37	10.37
10.38	10.38
10.39	10.39
10.40	10.40
10.41	10.41
10.42	10.42
10.43	10.43
10.44	10.44
10.45	10.45
10.46	10.46
10.47	10.47
10.48	10.48
10.49	10.49
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10.54	10.54
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10.56	10.56
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10.60	10.60
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10.91	10.91
10.92	10.92
10.93	10.93
10.94	10.94
10.95	10.95
10.96	10.96
10.97	10.97
10.98	10.98
10.99	10.99
11.00	11.00

[illegible]

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRHLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRGTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVWRWTKQNLD
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLFPDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515